SEQUENCE LISTING <110> CANFIELD, WILLIAM M <120> METHODS FOR PRODUCING HIGHLY PHOSPHORYLATED LYSOSOMAL HYDROLASES <130> 210119US0CONT <150> 60/153,831 <151> 1999-09-14 <150> US 09/635,872 <151> 2000-08-10 <160> 52 <170> PatentIn version 3.1 <210> 1 <211> 928 <212> PRT <213> Homo sapiens <400> 1

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Ser Ala Phe Gln Phe Gly Glu Val Val Leu Glu Trp Ser Arg Asp Gln 35 40 45

Tyr His Val Leu Phe Asp Ser Tyr Arg Asp Asn Ile Ala Gly Lys Ser 50 55 60

Phe Cln Asn Arg Leu Cys Leu Pro Met Pro Ile Asp Val Val Tyr Thr 65 70 75 80

Trp 🗓 Asn Gly Thr Asp Leu Glu Leu Lys Glu Leu Gln Gln Val

Arg Glu Gln Met Glu Glu Glu Gln Lys Ala Met Arg Glu Ile Leu Gly
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Lys Asn Thr Thr Glu Pro Thr Lys Lys Ser Glu Lys Gln Leu Glu Cys
115 120 125

Leu Thr His Cys Ile Lys Val Pro Met Leu Val Leu Asp Pro Ala

Leu Pro Ala Asn Ile Thr Leu Lys Asp Val Pro Ser Leu Tyr Pro Ser 145 150 155 160

Phe His Ser Ala Ser Asp Ile Phe Asn Val Ala Lys Pro Lys Asn Pro 165 170 175

Ser Thr Asn Val Ser Val Val Val Phe Asp Ser Thr Lys Asp Val Glu 180 185 190

Asp Ala His Ser Gly Leu Leu Lys Gly Asn Ser Arg Gln Thr Val Trp 195 200 205

Arg Gly Tyr Leu Thr Thr Asp Lys Glu Val Pro Gly Leu Val Leu Met 210 215 220

Gln Asp Leu Ala Phe Leu Ser Gly Phe Pro Pro Thr Phe Lys Glu Thr

Asn Gln Leu Lys Thr Lys Leu Pro Glu Asn Leu Ser Ser Lys Val Lys 245 250 255

Leu Leu Gln Leu Tyr Ser Glu Ala Ser Val Ala Leu Leu Lys Leu Asn 260 265 270

Asn Pro Lys Asp Phe Gln Glu Leu Asn Lys Gln Thr Lys Lys Asn Met 275 280 285

Thr Ile Asp Gly Lys Glu Leu Thr Ile Ser Pro Ala Tyr Leu Leu Trp 290 295 300

Asp Leu Ser Ala Ile Ser Gln Ser Lys Gln Asp Glu Asp Ile Ser Ala 305 310 315 320

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Glm Ile Pro Ser Trp Leu Asn Leu Asp Asn Pro Arg Val Thr Ile Val

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360
365

The His Gln Asp Val Phe Arg Asn Leu Ser His Leu Pro Thr Phe Ser 370 380

Ser Pro Ala Ile Glu Ser His Ile His Arg Ile Glu Gly Leu Ser Gln 385 390 395 400

Lys Phe Ile Tyr Leu Asn Asp Asp Val Met Phe Gly Lys Asp Val Trp 405 410 415

Pro Asp Asp Phe Tyr Ser His Ser Lys Gly Gln Lys Val Tyr Leu Thr 420 425 430

Trp Pro Val Pro Asn Cys Ala Glu Gly Cys Pro Gly Ser Trp Ile Lys 435 440 445

Asp Gly Tyr Cys Asp Lys Ala Cys Asn Asn Ser Ala Cys Asp Trp Asp 450 455 460

Gly Gly Asp Cys Ser Gly Asn Ser Gly Gly Ser Arg Tyr Ile Ala Gly 465 470 470 475 480

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Lys Asp Ala Gln Leu Ser Leu Asn Thr Leu Asp Leu Gln Leu Glu His 705 710 715 720

Gly Asp Ile Thr Leu Lys Gly Tyr Asn Leu Ser Lys Ser Ala Leu Leu 725 730 735

Arg Ser Phe Leu Met Asn Ser Gln His Ala Lys Ile Lys Asn Gln Ala 740 745 750

Ile Ile Thr Asp Glu Thr Asn Asp Ser Leu Val Ala Pro Gln Glu Lys 755 760 765

Gln Val His Lys Ser Ile Leu Pro Asn Ser Leu Gly Val Ser Glu Arg 770 780

Leu Gln Arg Leu Thr Phe Pro Ala Val Ser Val Lys Val Asn Gly His 785 790 795 800

Asp Gln Gly Gln Asn Pro Pro Leu Asp Leu Glu Thr Thr Ala Arg Phe 805 810 815

Arg Val Glu Thr His Thr Gln Lys Thr Ile Gly Gly Asn Val Thr Lys 820 825 830

Glu Glu Ser Pro Pro Ser Leu Ile Val Pro Leu Glu Ser Gln Met Thr Lys

835
840
845

Glu Lys Lys Ile Thr Gly Lys Glu Lys Glu Asn Ser Arg Met Glu Glu 850 860

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Leu Gln His Tyr Thr Asp Ser Tyr Leu Gly Phe Leu Pro Trp Glu Lys 885 890 895

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Ile Asp Arg Ile Val Met Gl<br/>n Glu Leu Gl<br/>n Asp Met Phe Pro Glu Glu 35  $\phantom{\bigg|}40\phantom{\bigg|}40\phantom{\bigg|}45\phantom{\bigg|}$ 

Phe Asp Lys Thr Ser Phe His Lys Val Arg His Ser Glu Asp Met Gln Phe Ala Phe Ser Tyr Phe Tyr Tyr Leu Met Ser Ala Val Gln Pro Leu 70 Asn Ile Ser Gln Val Phe Asp Glu Val Asp Thr Asp Gln Ser Gly Val Leu Ser Asp Arg Glu Ile Arg Thr Leu Ala Thr Arg Ile His Glu Leu 105 Pro Leu Ser Leu Gln Asp Leu Thr Gly Leu Glu His Met Leu Ile Asn 120 Cys Ser Lys Met Leu Pro Ala Asp Ile Thr Gln Leu Asn Asn Ile Pro **□**<sup>130</sup> 135 ╝ Pro節Thr Gln Glu Ser Tyr Tyr Asp Pro Asn Leu Pro Pro Val Thr Lys U Ser Leu Val Thr Asn Cys Lys Pro Val Thr Asp Lys Ile His Lys Ala 170 ΠU Tyr Lys Asp Lys Asn Lys Tyr Arg Phe Glu Ile Met Gly Glu Glu 185 180 ٦. Ile Ala Phe Lys Met Ile Arg Thr Asn Val Ser His Val Val Gly Gln 200 Leu Asp Asp Ile Arg Lys Asn Pro Arg Lys Phe Val Cys Leu Asn Asp 210 215 220 Asn Ile Asp His Asn His Lys Asp Ala Gln Thr Val Lys Ala Val Leu 225 230 Arg Asp Phe Tyr Glu Ser Met Phe Pro Ile Pro Ser Gln Phe Glu Leu 245 250

Pro Arg Glu Tyr Arg Asn Arg Phe Leu His Met His Glu Leu Gln Glu
260 265 270

Trp Arg Ala Tyr Arg Asp Lys Leu Lys Phe Trp Thr His Cys Val Leu 275 280 285

Ala Thr Leu Ile Met Phe Thr Ile Phe Ser Phe Phe Ala Glu Gln Leu 290 295 300

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10 45

Leu Gln Ala Lys Arg Asp Pro Ser Pro Val Ser Gly Pro Val His Leu 50 55 60

Phe Arg Leu Ser Gly Lys Cys Phe Ser Leu Val Glu Ser Thr Tyr Lys 65 70 75 80

Tyr Clu Phe Cys Pro Phe His Asn Val Thr Gln His Glu Gln Thr Phe
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Ile Ala Asn Asn Thr Phe Thr Gly Met Trp Met Arg Asp Gly Asp Ala 115 120 125

Cys Arg Ser Arg Ser Arg Gln Ser Lys Val Glu Leu Ala Cys Gly Lys 130 135 140

Ser Asn Arg Leu Ala His Val Ser Glu Pro Ser Thr Cys Val Tyr Ala 145 150 155 160

Leu Thr Phe Glu Thr Pro Leu Val Cys His Pro His Ala Leu Leu Val 165 170 175

Tyr Pro Thr Leu Pro Glu Ala Leu Gln Arg Gln Trp Asp Gln Val Glu 180 185 190

Gln Asp Leu Ala Asp Glu Leu Ile Thr Pro Gln Gly His Glu Lys Leu Leu Arg Thr Leu Phe Glu Asp Ala Gly Tyr Leu Lys Thr Pro Glu Glu 215 Asn Glu Pro Thr Gln Leu Glu Gly Gly Pro Asp Ser Leu Gly Phe Glu 230 235 240 Thr Leu Glu Asn Cys Arg Lys Ala His Lys Glu Leu Ser Lys Glu Ile 245 Lys Arg Leu Lys Gly Leu Leu Thr Gln His Gly Ile Pro Tyr Thr Arg Pro Thr Glu Thr Ser Asn Leu Glu His Leu Gly His Glu Thr Pro Arg Ø Ala thys Ser Pro Glu Gln Leu Arg Gly Asp Pro Gly Leu Arg Gly Ser 290 295 300 Uī Leu 305 N 4 <211> 5597 <212> DNA <213> Homo sapiens <400> 4 <210> 60 cggagccag cgggcgtccg tcgccggagc tgcaatgagc ggcgcccgga ggctgtgacc 120 tgcg by ggcccgaccg gggcccctga atggcggctc gctgaggcgg cggcggcggc ggcggttcag gctcctcggg gcgtggcgtg gcggtgaagg ggtgatgctg ttcaagctcc 180 tgca<sup>i</sup>gagaca aacctatacc tgcctgtccc acaggtatgg gctctacgtg tgcttcttgg 240 gegtegttgt caccategte teegeettee agtteggaga ggtggttetg gaatggagee 300 gagatcaata ccatgttttg tttgattcct atagagacaa tattgctgga aagtcctttc 360 420 agaatcggct ttgtctgccc atgccgattg acgttgttta cacctgggtg aatggcacag atcttgaact actgaaggaa ctacagcagg tcagagaaca gatggaggag gagcagaaag 480 caatgaqaga aatccttggg aaaaacacaa cggaacctac taagaagagt gagaagcagt 540 600 tagaqtqttt qctaacacac tqcattaaqq tqccaatqct tqtactqqac ccaqccctqc cagccaacat caccctgaag gacgtgccat ctctttatcc ttctttcat tctgccagtg 660 acattttcaa tgttgcaaaa ccaaaaaacc cttctaccaa tgtctcagtt gttgtttttg 720 acagtactaa ggatgttgaa gatgcccact ctggactgct taaaggaaat agcagacaga 780

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Pro Pro Pro Pro Ala Thr Pro Gly Ala Gly Gly Leu Ala Val Arg Thr 65 70 75 80

Phe Val Ser His Phe Arg Asp Arg Ala Val Ala Gly His Leu Thr Arg 85 90 95

Ala Val Glu Pro Leu Arg Thr Phe Ser Val Leu Glu Pro Gly Gly Pro 100 105 110

Gly Gly Cys Ala Ala Arg Arg Arg Ala Thr Val Glu Glu Thr Ala Arg 115 120 125

Ala Ala Asp Cys Arg Val Ala Gln Asn Gly Gly Phe Phe Arg Met Asn 130 135 140

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Ser Teu Val Thr Asn Cys Lys Pro Val Thr Asp Lys Ile His Lys Ala

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Ile tala Phe Lys Met Ile Arg Thr Asn Val Ser His Val Val Gly Gln
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Asn Ile Asp His Asn His Lys Asp Ala Arg Thr Val Lys Ala Val Leu 225 230 235 240

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Pro Arg Glu Tyr Arg Asn Arg Phe Leu His Met His Glu Leu Gln Glu 260 265 270

Trp Arg Ala Tyr Arg Asp Lys Leu Lys Phe Trp Thr His Cys Val Leu 275 280 285

Ala Thr Leu Ile Ile Phe Thr Ile Phe Ser Phe Phe Ala Glu Gln Ile 290 295 300

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Leu Thr Phe Glu Thr Pro Leu Val Cys His Pro His Ser Leu Leu Val 165 170 175

Tyr Pro Thr Leu Ser Glu Ala Leu Gln Gln Arg Leu Asp Gln Val Glu 180 185 190

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25 20 30

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Lys Esn Thr Thr Glu Pro Thr Lys Lys Ser Glu Lys Gln Leu Glu Cys 115 120 Ō

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Leu 🏗 o Ala Thr Ile Thr Leu Lys Asp Leu Pro Thr Leu Tyr Pro Ser 145 ≡ 150 155

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Ser Phr Asn Val Pro Val Val Val Phe Asp Thr Thr Lys Asp Val Glu

Asp Ala His Ala Gly Pro Phe Lys Gly Gln Gln Thr Asp Val Trp 195 200

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Lys Leu Leu Arg Leu Tyr Ser Glu Ala Ser Val Ala Leu Leu Lys Leu 265

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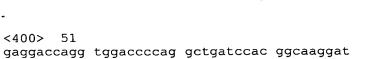
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